CLAIM SUMMARY DOCUMENT

Claim 1 (Currently amended) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a ~~eucaryotic~~ plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in said ~~eucaryotic~~ plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest

wherein said DNA region comprises an intron sequence heterologous to said sense sequence; and

c) a DNA region involved in transcription termination and polyadenylation; ~~wherein said DNA region, which when transcribed yields said RNA molecule, comprises a heterologous sequence~~.

Claim 2 (Currently amended) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a ~~eucaryotic~~ plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in said ~~eukaryotic~~ plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence

wherein said DNA region comprises an intron sequence heterologous to said sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation~~;~~

~~wherein said DNA region, which when transcribed yields said RNA molecule, comprises a heterologous intron sequence~~.

Claim 3 (Original) The method of claim 2, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequence.

Claim 4 (Previously amended) The method of claim 2, wherein said sense nucleotide sequence comprises at least about 550 consecutive nucleotides having between 75% and 100% sequence identity with at least about 550 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest.

Claim 5 (Currently amended) The method of claim 2, wherein said nucleic acid of interest is a

gene integrated in the genome of said ~~eucaryotic~~ plant cell.

Claim 6 (Original) The method of claim 5, wherein said gene is an endogenous gene

Claim 7 (Original) The method of claim 5, wherein said gene is a foreign transgene.

Claim 8 (Currently amended) The method of claim 2, wherein said chimeric DNA is stably integrated in the genome of said ~~eucaryotic~~ plant cell.

Claim 9 (Original) The method of claim 2, wherein said nucleic acid of interest is comprised in the genome of an infecting virus.

Claim 10 (Original) The method of claim 9, wherein said infecting virus is an RNA virus.

Claim 11 (Canceled)

Claim 12. (Currently amended) The method of claim ~~11~~ 2, wherein said plant cell is comprised within a plant.

Claims 13-21. (Withdrawn)

Claim 22. (Currently amended) A ~~eucaryotic~~ plant cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said ~~eucaryotic~~ plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i. a sense nucleotide sequence including at least 10 consecutive nucleotides having between 75 and 100% sequence identity with at least

10 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii. an antisense nucleotide sequence including at least 10 consecutive nucleotides, having between about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence

wherein said DNA region comprises an intron sequence heterologous to said sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation~~;~~

~~wherein said DNA region, which when transcribed yields said RNA molecule, comprises a heterologous intron sequence~~.

Claims 23-24. (Withdrawn)

Claim 25 (Canceled)

Claim 26 (Currently amended) A plant comprising the plant cell of claim ~~25~~ 22.

Claims 27-38. (Withdrawn)

Claim 39 (Canceled)

Claim 40. (Previously amended) The method of claim 2, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 41(Canceled)

Claim 42 (Currently amended) The ~~eucaryotic~~ plant cell of claim 22, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields encoding said antisense nucleotide sequence.

Claim 43 (Original) The method of claim 2, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

Claim 44 (Original) The method of claim 2, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 45 (Canceled)

Claim 46 (Original) The method of claim 45, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

Claims 47-49 (Canceled)

Claim 50 (Previously amended) The method of claim 44, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 51-52 (Canceled)

Claim 53. (Currently amended) The ~~eucaryotic~~ plant cell of claim 22, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

Claim 54 (Currently amended) The ~~eucaryotic~~ plant cell of claim 22, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 55 (Canceled)

Claim 56 (Currently amended) The ~~eucaryotic~~ plant cell of claim 53, wherein said intron is located between part of said DNA region which when transcribed yields said sense

nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 57 (Canceled)

Claim 58 (Currently amended) The ~~eucaryotic~~ plant cell of claim 54, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 59-62 (Canceled)

Claim 63 (New) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest

wherein said DNA region comprises an intron sequence heterologous to said sense sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 64 (New) A chimeric DNA comprising the following operably linked parts:

a.) a promoter, operative in a plant cell;

b.) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i.) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii.) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence,

wherein said DNA region comprises an intron sequence heterologous to said region with sense nucleotide sequence; and

c.) a DNA region involved in transcription termination and polyadenylation.

Claim 65 (New) The chimeric DNA of claim 64, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 66 (New) The chimeric DNA of claim 64, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20 consecutive nucleotides, having about 75% to about 100% sequence identity with the

complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

Claim 67 (New) The chimeric DNA of claim 64, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 68 (New) The chimeric DNA of claim 66, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 69 (New) The chimeric DNA of claim 67, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 70 (New) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the

hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

wherein said DNA region comprises an intron sequence heterologous to said sense sequence; and

c) a DNA region involved in transcription termination and polyadenylation;

Claim 71 (New) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a.) a promoter, operative in a eukaryotic cell;

b.) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i.) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and

ii.) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive

nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence

wherein said DNA region comprises an intron sequence heterologous to said region with sense nucleotide sequence; and

c.) a DNA region involved in transcription termination and polyadenylation.

Claim 72 (New) The method of claim 71, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequence.

Claim 73 (New) The method of claim 71, wherein said sense nucleotide sequence comprises at least about 550 consecutive nucleotides having between 75% and 100% sequence identity with at least about 550 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest.

Claim 74 (New) The method of claim 71, wherein said nucleic acid of interest is a gene integrated in the genome of said eukaryotic cell.

Claim 75 (New) The method of claim 74, wherein said gene is an endogenous gene.

Claim 76 (New) The method of claim 74, wherein said gene is a foreign transgene.

Claim 77 (New) The method of claim 71, wherein said chimeric DNA is stably integrated in the genome of said eukaryotic cell.

Claim 78 (New) The method of claim 71, wherein said nucleic acid of interest is comprised in the genome of an infecting virus.

Claim 79 (New) The method of claim 78, wherein said infecting virus is an RNA virus.

Claim 80 (New) The method of claim 71, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 81 (New) The method of claim 71, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

Claim 82 (New) The method of claim 71, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 83 (New) The method of claim 81, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

Claim 84 (New) The method of claim 82, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 85 (New) An isolated eukaryotic cell, comprising a nucleic acid of interest, which is

normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i. a sense nucleotide sequence including at least 10 consecutive nucleotides having between 75 and 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii. an antisense nucleotide sequence including at least 10 consecutive nucleotides, having between about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence;

wherein said DNA region comprises an intron sequence heterologous to said region with sense nucleotide sequence; and

d) a DNA region involved in transcription termination and polyadenylation.

Claim 86 (New) The eukaryotic cell of claim 85, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields encoding said antisense nucleotide sequence.

Claim 87 (New) The eukaryotic cell of claim 85, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20

consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

Claim 88 (New) The eukaryotic cell of claim 85, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 89 (New) The eukaryotic cell of claim 87, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 90 (New) The eukaryotic cell of claim 88, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 91(New) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of

interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

wherein said DNA region comprises an intron sequence heterologous to said sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation;

Claim 92. (New) A chimeric DNA comprising the following operably linked parts:

a.) a promoter, operative in a eukaryotic cell;

b.) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i.) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii.) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence;

wherein said DNA region comprises an intron sequence heterologous to said region with sense nucleotide sequence; and

c.) a DNA region involved in transcription termination and polyadenylation.

Claim 93. (New) The chimeric DNA of claim 92, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 94 (New) The chimeric DNA of claim 92, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

Claim 95 (New) The chimeric DNA of claim 92, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 96 (New) The chimeric DNA of claim 94, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 97 (New) The chimeric DNA of claim 95, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide

sequence.

Claim 98 (New) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

d) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest;

wherein said DNA region comprises an intron sequence; and

e) a DNA region involved in transcription termination and polyadenylation.

Claim 99. (New) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell, a chimeric DNA comprising the following operably linked parts:

a.) a promoter, operative in said plant cell;

b.) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i.) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of

said nucleic acid of interest; and

ii.) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence;

wherein said DNA region comprises an intron sequence; and

c.) a DNA region involved in transcription termination and polyadenylation.

Claim 100. (New) A plant cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i. a sense nucleotide sequence including at least 10 consecutive nucleotides having between 75 and 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii. an antisense nucleotide sequence including at least 10 consecutive nucleotides, having between about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and

antisense nucleotide sequence;

wherein said DNA region comprises an intron sequence; and

e) a DNA region involved in transcription termination and polyadenylation.

Claim 101 (New) A plant comprising the plant cell of claim 100.

Claim 102. (New) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest; and

c) a DNA region involved in transcription termination and polyadenylation;

wherein said DNA region comprises an intron sequence.

Claim 103. (New) A chimeric DNA comprising the following operably linked parts:

a.) a promoter, operative in a plant cell;

b.) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i.) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii.) an antisense nucleotide sequence including at least 10 consecutive

nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence;

wherein said DNA region comprises an intron sequence; and

c.) a DNA region involved in transcription termination and polyadenylation.

Claim 104. (New) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest;

wherein said DNA region comprises an intron sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 105 (New) A method for reducing the phenotypic expression of a nucleic acid of interest,

which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a.) a promoter, operative in a eukaryotic cell;

b.) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i.) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and

ii.) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence;

wherein said DNA region comprises an intron sequence; and

c.) a DNA region involved in transcription termination and polyadenylation.

Claim 106 (New) An isolated eukaryotic cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i. a sense nucleotide sequence including at least 10 consecutive

nucleotides having between 75 and 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii. an antisense nucleotide sequence including at least 10 consecutive nucleotides, having between about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence;

wherein said DNA region comprises an intron sequence; and

f) a DNA region involved in transcription termination and polyadenylation.

Claim 107 (New) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest;

wherein said DNA region comprises an intron; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 108. (New) A chimeric DNA comprising the following operably linked parts:

a.) a promoter, operative in a eukaryotic cell;

b.) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i.) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii.) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence;

wherein said DNA region comprises an intron sequence; and

c.) a DNA region involved in transcription termination and polyadenylation.